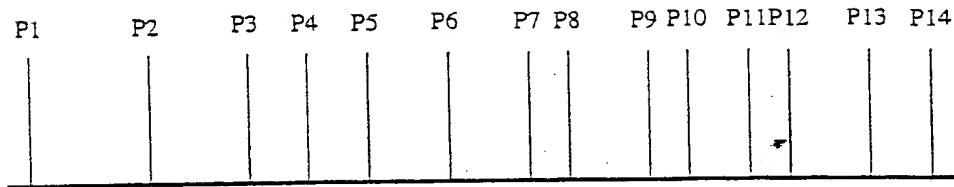
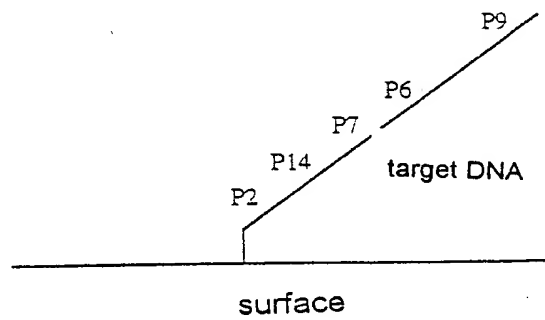


1. Mass distribution of the probes



2. Hybridization



3. Mass distribution of the hybridized probes

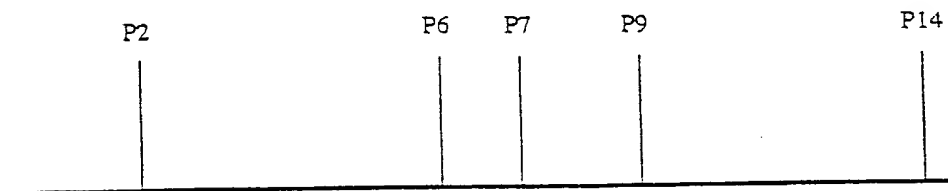
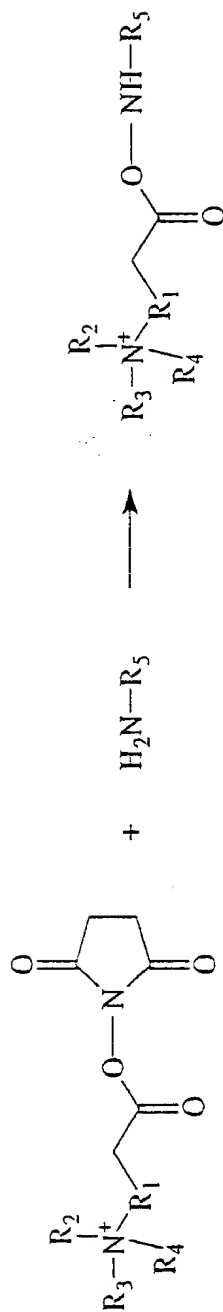


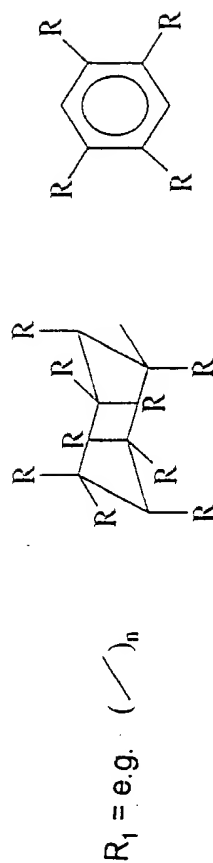
Fig. 1

N-terminal mass/charge tagging

Fig. 2



R = e.g. alkyl, -CH₃, -C₂H₅, -C₃H₇, -C₄H₉ etc.



R₂₋₄ = e.g. alkyl, substituted alkyl

R₅ = e.g. nucleic acid, PNA, methyl phosphonate nucleic acid, phosphorothioate nucleic acid

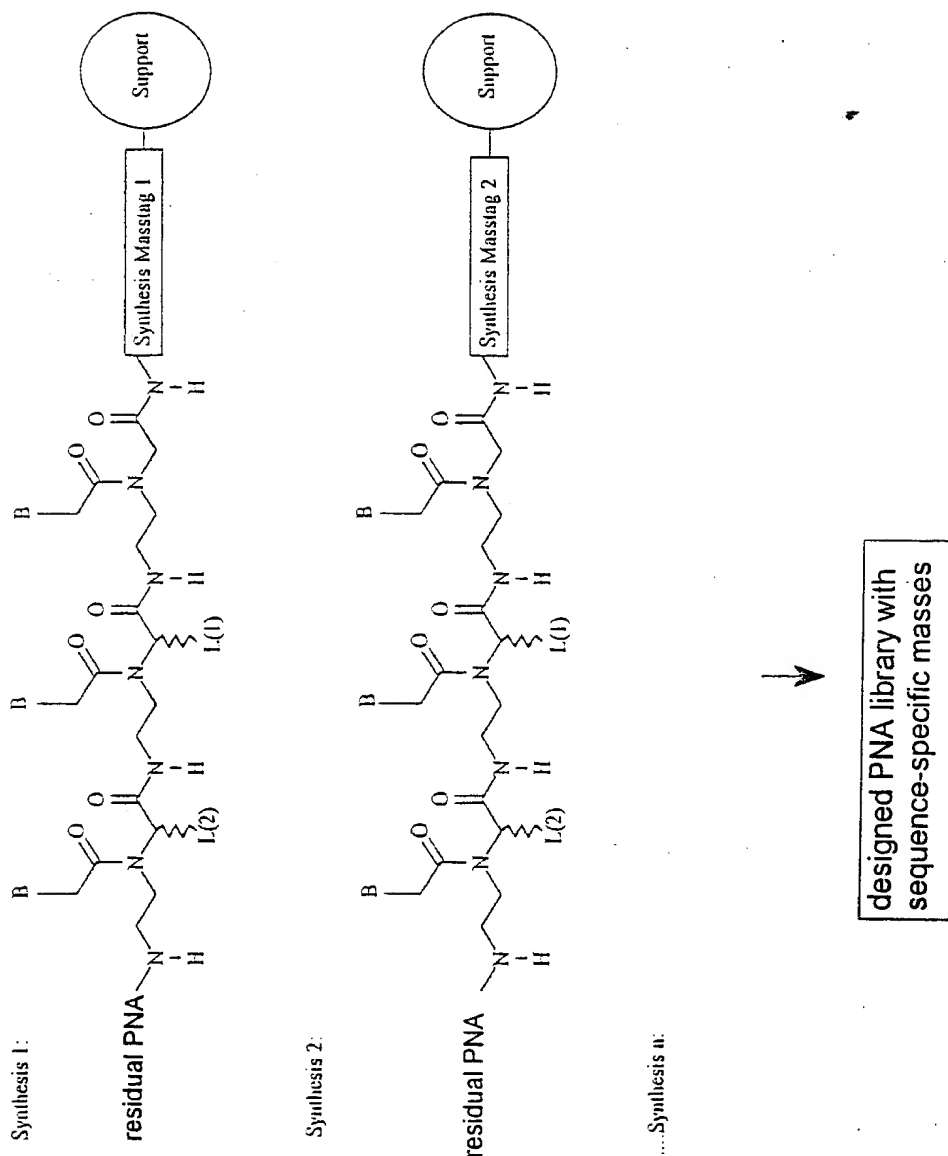


Fig. 3

B = adenine, cytosine, guanine, thymine or purine or pyrimidine derivatives or their deaza analogues

L(n) are various sets of substituents, selected specifically for each base, which are inserted in each synthesis step in order to obtain minimized peak overlaps in the MALDI-MS.

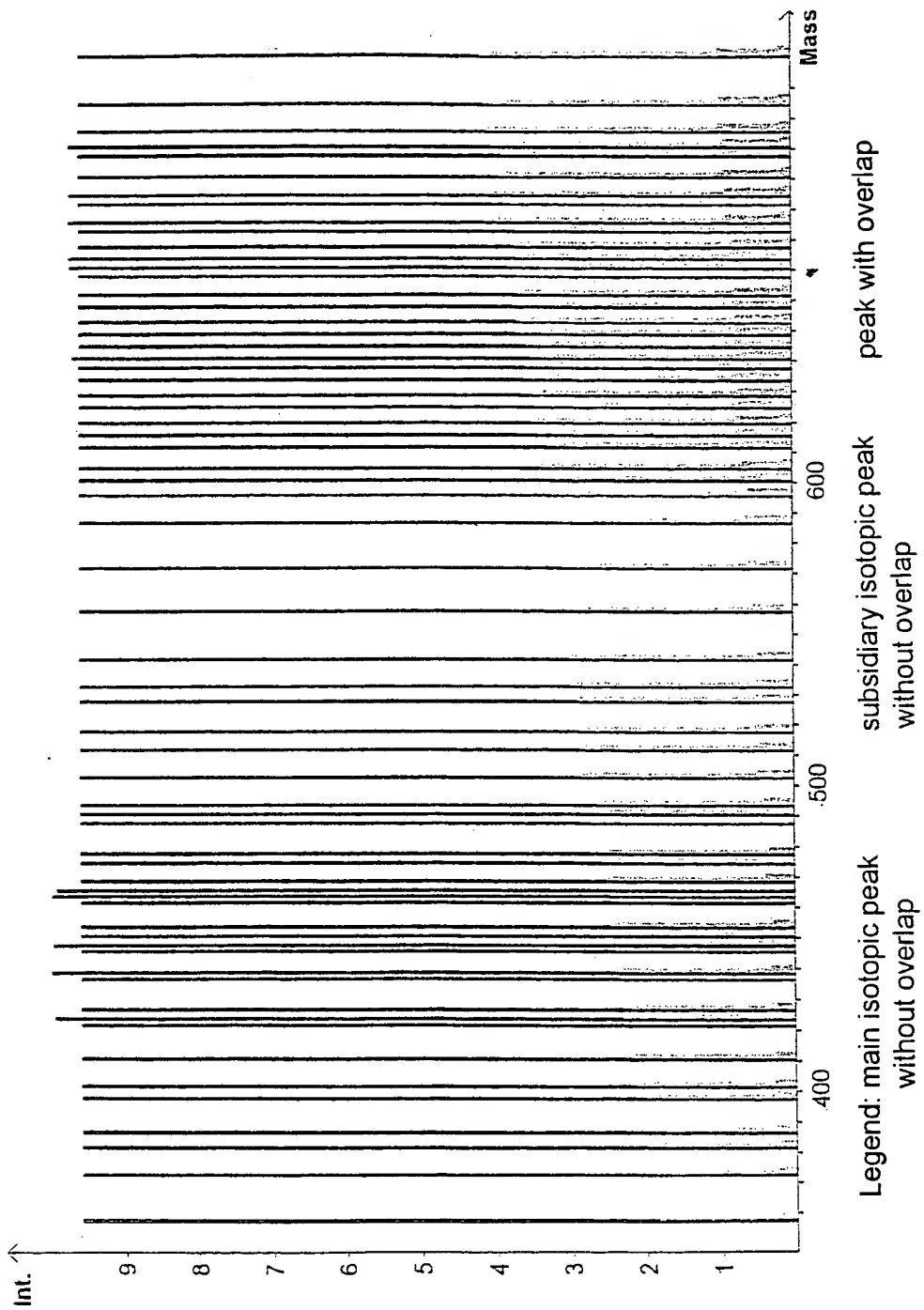


Fig. 4

64 mass peaks corresponding to a specific PNA sequence;
mass tagging

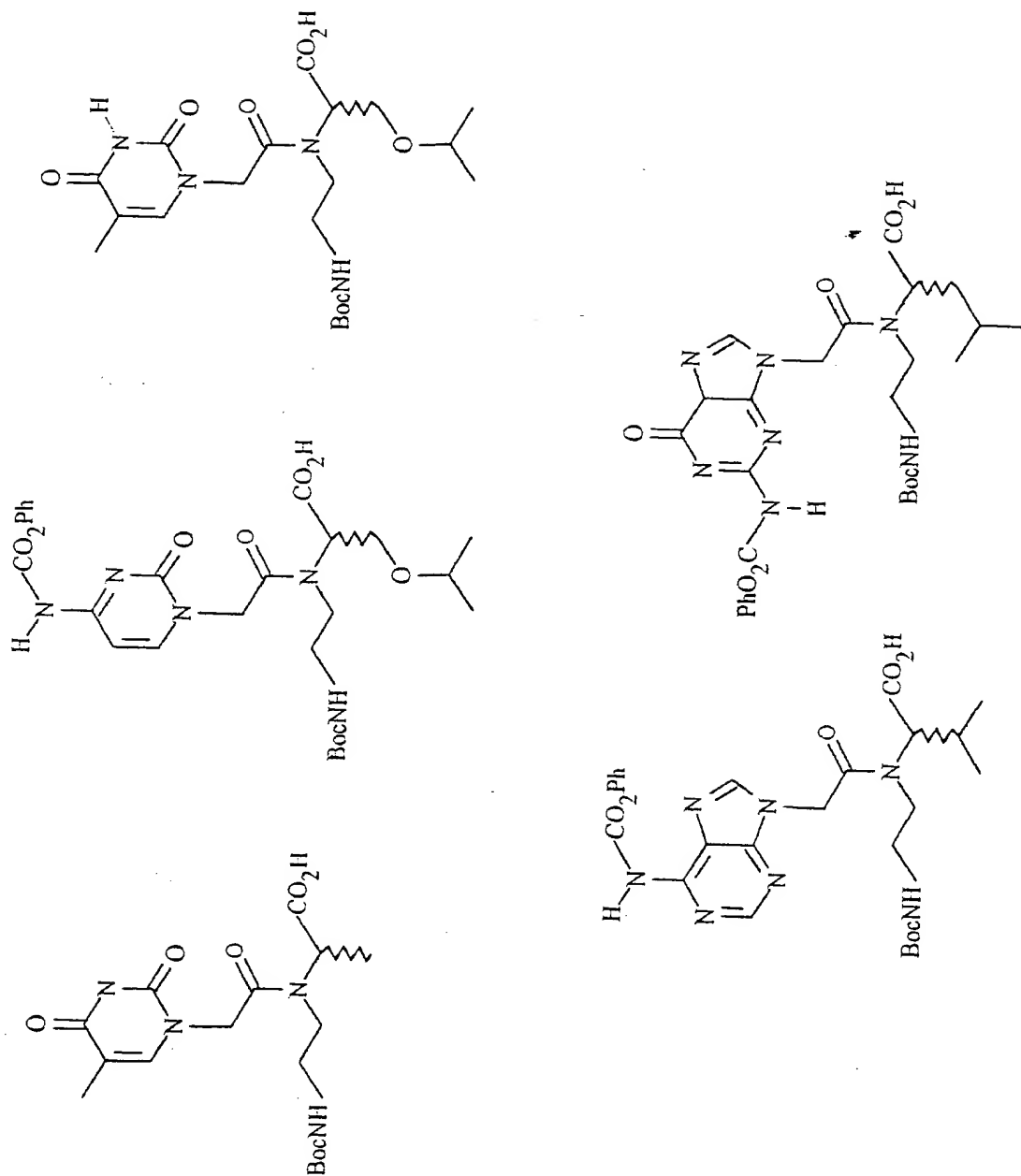


Fig. 5

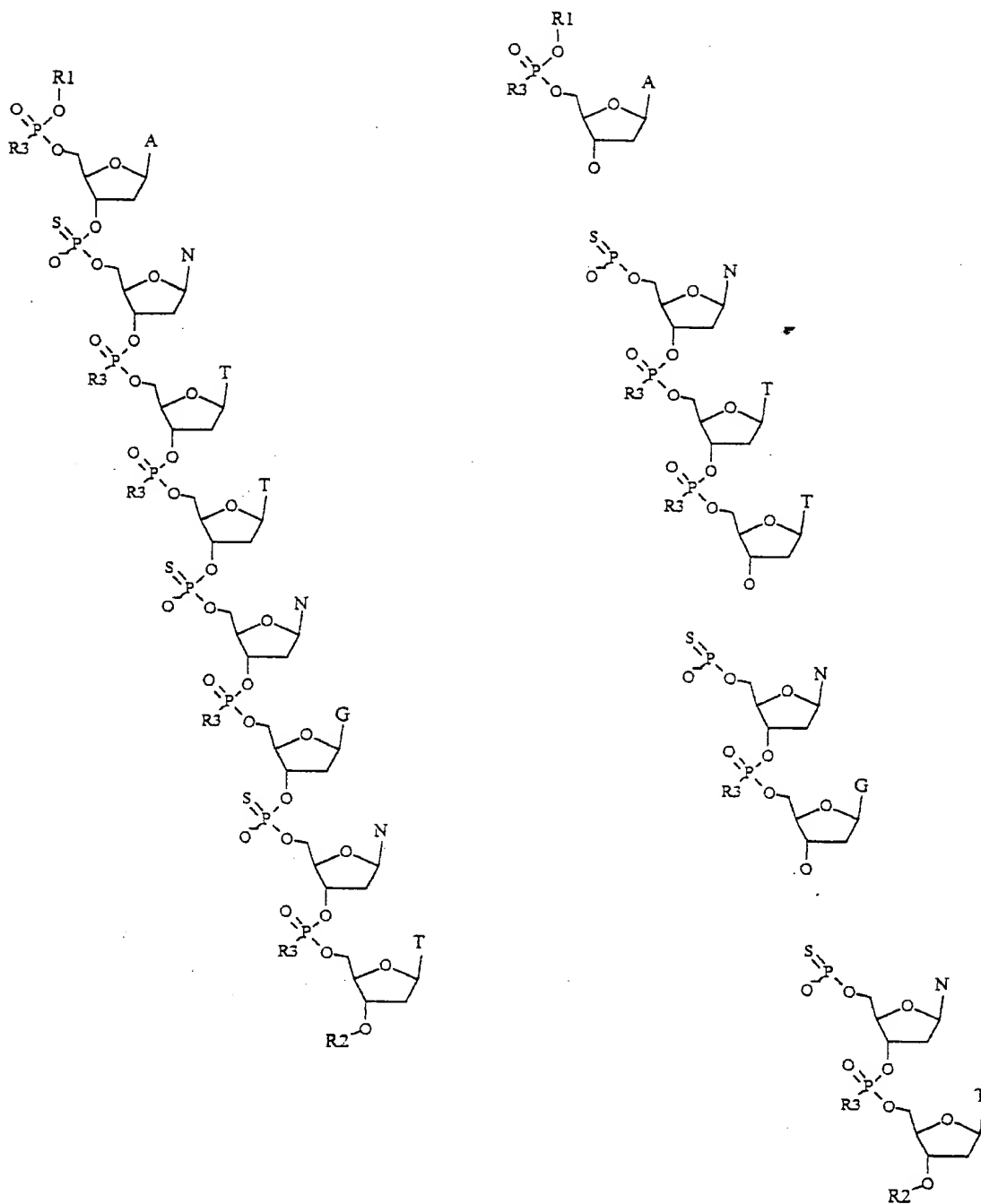


Fig. 6